

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/547, 530  
Source: PCT  
Date Processed by STIC: 09/13/2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,530

TIME: 10:10:08

Input Set : A:\Sequence Listings.ST25.txt

Output Set: N:\CRF4\09132005\J547530.raw

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3 <110> APPLICANT: Regents of the University of California, The
4     Leonard, Rome H.
5     Valerie, Kickhoefer A.
6     Sujna, Raval-Fernandes
7     Phoebe, Stewart L.
9 <120> TITLE OF INVENTION: Vault and Vault-like Carrier Molecules
11 <130> FILE REFERENCE: 14399-1EP
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/547,530
C--> 14 <141> CURRENT FILING DATE: 2005-08-31
16 <150> PRIOR APPLICATION NUMBER: 60/453,800
17 <151> PRIOR FILING DATE: 2003-03-10
19 <150> PRIOR APPLICATION NUMBER: PCT/US04/07434
20 <151> PRIOR FILING DATE: 2004-03-10
22 <160> NUMBER OF SEQ ID NOS: 143
24 <170> SOFTWARE: PatentIn version 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 893
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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38          20          25          30
41 Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
42          35          40          45
45 Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
46          50          55          60
49 Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
50 65          70          75          80
53 Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
54          85          90          95
57 Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
58          100         105         110
61 Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
62          115         120         125
65 Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
66          130         135         140
69 Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
70 145         150         155         160
73 Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
74          165         170         175
77 Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr

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81 Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
82          195          200          205
85 Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
86          210          215          220
89 Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
90 225          230          235          240
93 Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
94          245          250          255
97 Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
98          260          265          270
101 Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
102          275          280          285
105 Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
106          290          295          300
109 Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
110 305          310          315          320
113 Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
114          325          330          335
117 Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
118          340          345          350
121 Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
122          355          360          365
125 Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
126          370          375          380
129 Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
130 385          390          395          400
133 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
134          405          410          415
137 Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
138          420          425          430
141 Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
142          435          440          445
145 Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
146          450          455          460
149 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
150 465          470          475          480
153 Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
154          485          490          495
157 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
158          500          505          510
161 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
162          515          520          525
165 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
166          530          535          540
169 Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
170 545          550          555          560
173 Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
174          565          570          575

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178          580          585          590
181 Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
182          595          600          605
185 Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
186          610          615          620
189 Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
190 625          630          635          640
193 Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
194          645          650          655
197 Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
198          660          665          670
201 Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
202          675          680          685
205 Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
206          690          695          700
209 Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
210 705          710          715          720
213 Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
214          725          730          735
217 Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
218          740          745          750
221 Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
222          755          760          765
225 Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
226          770          775          780
229 Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
230 785          790          795          800
233 Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
234          805          810          815
237 Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
238          820          825          830
241 Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
242          835          840          845
245 Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
246          850          855          860
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250 865          870          875          880
253 Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg
254          885          890
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258 <211> LENGTH: 2682
259 <212> TYPE: DNA
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262 <400> SEQUENCE: 2
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265 cagaacagca acgtgtcccg tgtggaggtc gggccaaaga cctacatccg gcaggacaat      120
267 gagagggtac tgtttgcccc catgcgcatg gtgaccgtcc cccacgtca ctactgcaca      180
269 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa      240

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271 gttcggcttc gccacgctga cctcgagatc cggctggccc aggacccctt cccctgtac 300
273 ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc 360
275 ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga 420
277 gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg 480
279 gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgaag 540
281 gagtgtctgg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca 600
283 gtaggggctg acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc 660
285 cttacggaaa agacagccct gcacctccgg gctcggcggg acttccggga cttcagggga 720
287 gtgtcccggc gactggggga ggagtggctg gtaacagtgc aggacacaga ggcccacgtg 780
289 ccagatgtcc acgaggagggt gctgggggtt gtgccatca ccaccctggg cccccacaac 840
291 tactgctga ttctcgacct gtgcggaccg gatggcaaga atcagctggg gcagaagcgc 900
293 gtggtcaagg gagagaagtc tttttctc cagccaggag agcagctgga acaaggcatc 960
295 caggatgtgt atgtgtgtc ggagcagcag gggctgtctc tgagggccct gcagcccctg 1020
297 gaggaggggg aggatgagga gaaggtctca caccaggctg gggaccactg gctcatccgc 1080
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349 aggggtggcca gtgggcccag ccctggggag gggatatccc ccagttctgc tcaggcccct 2640
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356 <212> TYPE: PRT
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365 Tyr Leu Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu

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366          20          25          30
369 Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile
370          35          40          45
373 Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile
374          50          55          60
377 Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser
378 65          70          75          80
381 Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys
382          85          90          95
385 Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu
386          100         105         110
389 Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp
390          115         120         125
393 Thr Val Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His
394          130         135         140
397 Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val
398 145         150         155         160
401 Gly Met Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser
402          165         170         175
405 Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu
406          180         185         190
409 Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser
410          195         200         205
413 Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys
414          210         215         220
417 Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu
418 225         230         235         240
421 Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser
422          245         250         255
425 Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala
426          260         265         270
429 Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg
430          275         280         285
433 Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val
434          290         295         300
437 Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met
438 305         310         315         320
441 Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys
442          325         330         335
445 Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu
446          340         345         350
449 Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn
450          355         360         365
453 Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His
454          370         375         380
457 Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu
458 385         390         395         400
461 Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg
462          405         410         415

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**VERIFICATION SUMMARY**

DATE: 09/13/2005

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Input Set : A:\Sequence Listings.ST25.txt

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date